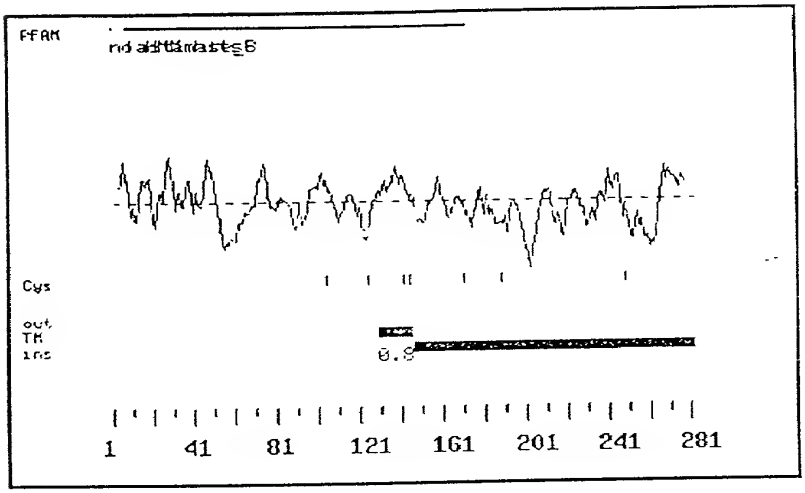
Input file Fbh50566FL.seq; Output File 50566.trans
Sequence length 1154

```
                                M   K   V   K   V   I   P   V   L   E   D   N   Y   M      14
CGGACGCGTGGGTCCGTGACC ATG AAG GTC AAG GTC ATC CCC GTG CTC GAG GAC AAC TAC ATG      42

 Y   L   V   I   E   E   L   T   R   E   A   V   A   V   D   V   A   V   P   K    34
TAC CTG GTC ATC GAG GAG CTC ACG CGC GAG GCG GTG GCC GTG GAC GTG GCT GTG CCC AAG   102

 R   L   L   E   I   V   G   R   E   G   V   S   L   T   A   V   L   T   T   H    54
AGG CTG CTG GAG ATC GTG GGC CGG GAG GGG GTG TCT CTG ACC GCT GTG CTG ACC ACC CAC   162

 H   H   W   D   H   A   R   G   N   P   E   L   A   R   L   R   P   G   L   A    74
CAT CAC TGG GAC CAC GCG CGG GGA AAC CCG GAG CTG GCG CGG CTT CGT CCC GGG CTG GCG   222

 V   L   G   A   D   E   R   I   F   S   L   T   R   R   L   A   H   G   E   E    94
GTG CTG GGC GCG GAC GAG CGC ATC TTC TCG CTG ACG CGC AGG CTG GCG CAC GGC GAG GAG   282

 L   R   F   G   A   I   H   V   R   C   L   L   T   P   G   H   T   A   G   H   114
CTG CGG TTC GGG GCC ATC CAC GTG CGT TGC CTC CTG ACG CCC GGC CAC ACC GCC GGC CAC   342

 M   S   Y   F   L   W   E   D   D   C   P   D   P   P   A   L   F   S   G   D   134
ATG AGC TAC TTC CTG TGG GAG GAC GAT TGC CCG GAC CCA CCC GCC CTG TTC TCG GGC GAC   402

 A   L   S   V   A   G   C   G   S   C   L   E   G   S   A   Q   Q   M   Y   Q   154
GCG CTG TCG GTG GCC GGC TGC GGC TCG TGC CTG GAG GGC AGC GCC CAG CAG ATG TAC CAG   462

 S   L   A   E   L   G   T   L   P   P   E   T   K   V   F   C   G   H   E   H   174
AGC CTG GCC GAG CTG GGT ACC CTG CCC CCC GAG ACG AAG GTG TTC TGC GGC CAC GAG CAC   522

 T   L   S   N   L   E   F   A   Q   K   V   E   P   C   N   D   H   V   R   A   194
ACG CTT AGC AAC CTG GAG TTT GCC CAG AAA GTG GAG CCC TGC AAC GAC CAC GTG AGA GCC   582

 K   L   S   W   A   K   K   R   D   E   D   D   V   P   T   V   P   S   T   L   214
AAG CTG TCC TGG GCT AAG AAG AGG GAT GAG GAT GAC GTG CCC ACT GTG CCG TCG ACT CTG   642

 G   E   E   R   L   Y   N   P   F   L   R   V   A   E   E   P   V   R   K   F   234
GGC GAG GAG CGC CTC TAC AAC CCC TTC CTG CGG GTG GCA GAG GAG CCG GTG CGC AAG TTC   702

 T   G   K   A   V   P   A   D   V   L   E   A   L   C   K   E   R   A   R   F   254
ACG GGC AAG GCG GTC CCC GCC GAC GTC CTG GAG GCG CTA TGC AAG GAG CGG GCG CGC TTC   762

 E   Q   A   G   E   P   R   Q   P   Q   A   R   A   L   L   A   L   Q   W   G   274
GAA CAG GCG GGC GAG CCG CGG CAG CCA CAG GCG CGG GCC CTC CTT GCG CTG CAG TGG GGG   822

 L   L   S   A   A   P   H   D   *                                               283
CTC CTG AGT GCA GCC CCA CAC GAC TGA                                             849

GCCACCCAGACCCTCACAGGGCTGGGGCCTGCGTCCCTCCTCGTGACCTCGGCCAGCTGGACCCACATGAGGGCCACCT

CTGGAACCTTCTTCGAGGCCCTGGCCAGCCATCTGCCCAGCCTCGGAGGGTGGGCAACCTGGTGCTTCCCGGGTGGACA

CACAGGACCACTCAGTGGGGCCTGTGTGGGCGCCGAGACCTGGGTGTCTGGGAAGTGGGGCACACGGGGCCTCCGAACT

ATGAATAAAGCTTTGAAAGCCGTTGTCAAAAAAAAAAAAAAAAAAA
```

FIGURE 1

Analysis of 50566 (282 aa)



>50566
MKVKVIPVLEDNYMYLVIEELTREAVAVDVAVPKRLLEIVGREGVSLTAVLTTHHHWDHA
RGNPELARLRPGLAVLGADERIFSLTRRLAHGEELRFGAIHVRCLLTPGHTAGHMSYFLW
EDDCPDPPALFSGDALSVAGCGSCLEGSAQQMYQSLAELGTLPPETKVFCGHEHTLSNLE
FAQKVEPCNDHVRAKLSWAKKRDEDDVPTVPSTLGEERLYNPFLRVAEEPVRKFTGKAVP
ADVLEALCKERARFEQAGEPRQPQARALLALQWGLLSAAPHD

Transmembrane Segments Predicted by MEMSAT

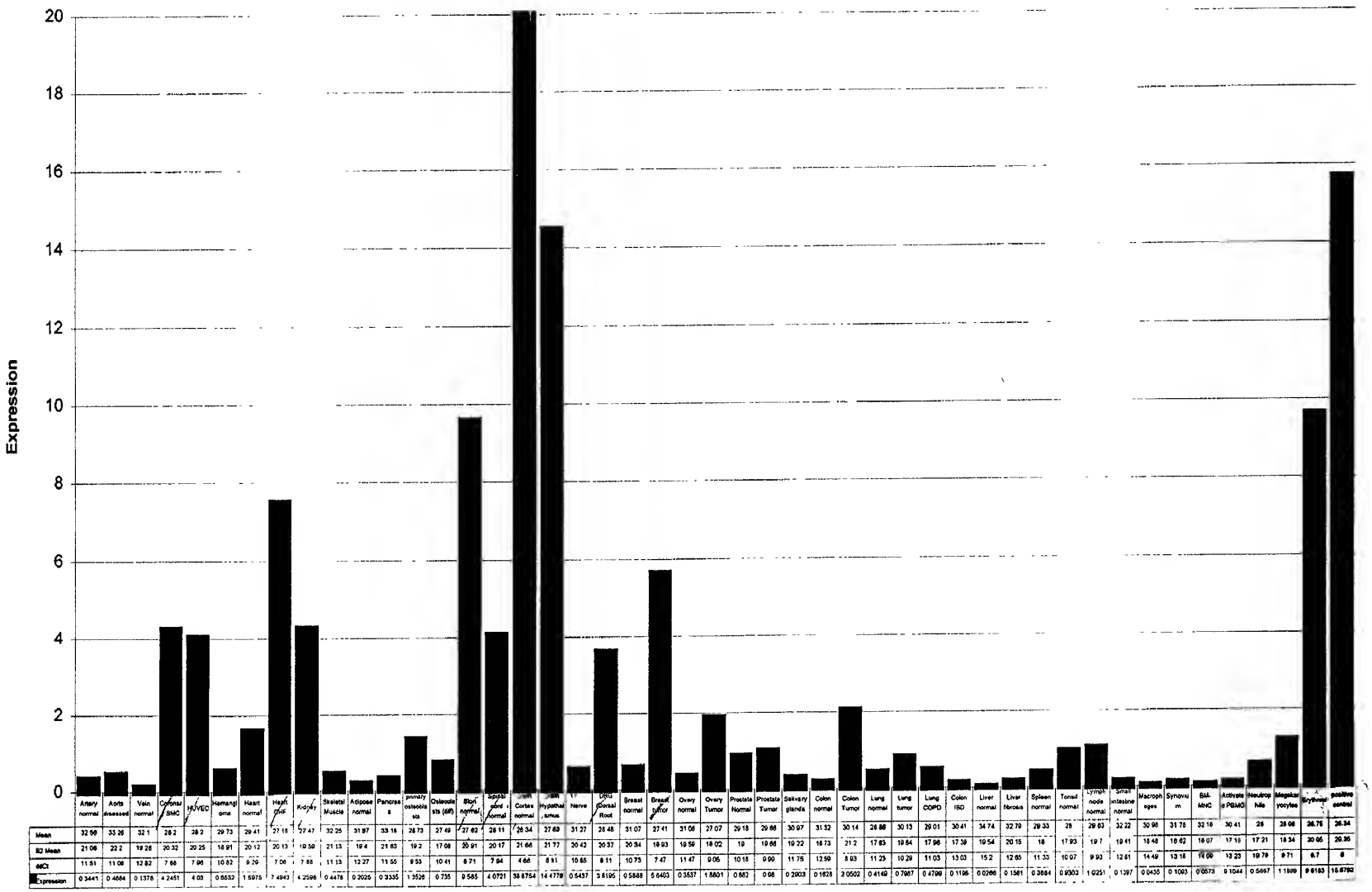
Start	End	Orient	Score
129	145	out-->ins	0.8

FIGURE 2

```
Scores for sequence family classification (score includes all domains):
Model       Description                                   Score    E-value  N
--------    -----------                                   -----    -------- ---
lactamase_B  Metallo-beta-lactamase superfamily            133.3    4.4e-36   1

Parsed for domains:
Model       Domain  seq-f seq-t    hmm-f hmm-t      score  E-value
--------    ------- ----- -----    ----- -----      -----  -------
lactamase_B   1/1       7   172 ..     1   218 []   133.3  4.4e-36

Alignments of top-scoring domains:
lactamase_B: domain 1 of 1, from 7 to 172: score 133.3, E = 4.4e-36
                   *->pglvdsnaylvedddggPgeaaliDpGttapaaeallrllkdggple
                      p l d+++ylv+ + +  +ea+ +D + +   +.++++ ++
       50566     7    PVLEDNYMYLVIEELT--REAVAVDVAVPKR-LLEIVGREG------ 44

                   nikkidaiilTHaHaDHiGGapaellekfgvpvaahaaevyaskdylgyg
                       ++a++ TH+H+DH+ G+p el+++ +      +  v       +++
       50566     45 --VSLTAVLTTHHHWDHARGNP-ELARLRP------GLAV-------LGA 78

                   edrlk..dealkdgdltflivieelrvglgvelevihtPGtHTpgsivyy
                   ++r+ + ++ l++g+         elr+g  ++++++ tPG HT g+++y+
       50566     79 DERIFslTRRLAHGE--------ELRFG-AIHVRCLLTPG-HTAGHMSYF 118

                   lpeekggespkivvLftGDtlfsggcpdgetdlplgrtdllggdpaelie
                   l+e+    +p   +Lf+GD+l  +gc         g    l+g++ +++
       50566    119 LWEDDCPDPP---ALFSGDALSVAGC---------GS--CLEGSAQQMYQ 154

                   sleqsesllkllpddtvvypGH<-*
                   sl     +l  +lp++t v++GH
       50566    155 SLA----ELG-TLPPETKVFCGH    172
```

FIGURE 3

38.8 **phase 1.6.8 of 50566.1**



	Artery normal	Aorta diseased	Vein normal	Coronar SMC	HUVEC	Hemangioma	Heart normal	Hepat ocyte	Kidney	Skeletal Muscle	Adipose normal	Pancreas	primary osteobla sts	Osteocla sts (diff)	Brain normal	Spinal cord normal	Brain Cortex normal	Brain Hypothal amus	T Nerve	DRG Dorsal Root	Breast normal	Breast tumor	Ovary normal	Ovary Tumor	Prostate Normal	Prostate Tumor	Salivary glands	Colon normal	Colon Tumor	Lung normal	Lung tumor	Lung COPD	Colon IBD	Liver normal	Liver fibrosis	Spleen normal	Tonsil normal	Lymph node normal	Small intestine normal	Macroph ages	Synoviu m	BM-MNC	Activate d PBMC	Neutrop hils	Megakar yocytes	Erythroid	positive control
Mean	32.56	33.26	32.1	28.2	28.2	29.73	29.41	27.15	27.47	32.25	31.87	33.18	28.73	27.49	27.62	28.11	26.34	27.69	31.27	28.48	31.07	27.41	31.06	27.07	29.18	29.66	30.97	31.32	30.14	28.88	30.13	29.01	30.41	34.74	32.79	29.33	28	29.63	32.22	30.98	31.76	32.16	30.41	28	28.06	26.75	26.34
B2 Mean	21.06	22.2	19.26	20.32	20.25	18.91	20.12	20.13	19.59	21.13	19.4	21.63	19.2	17.08	20.91	20.17	21.66	21.77	20.42	20.37	20.34	19.93	19.59	18.02	19	19.66	19.22	18.73	21.2	17.65	19.64	17.98	17.39	19.54	20.15	18	17.93	19.7	19.41	18.48	18.62	18.07	17.19	17.21	18.54	20.05	20.35
delCt	11.51	11.06	12.82	7.88	7.96	10.82	9.29	7.08	7.88	11.13	12.27	11.55	9.53	10.41	6.71	7.94	4.66	5.91	10.85	8.11	10.73	7.47	11.47	9.06	10.18	9.99	11.75	12.59	8.93	11.25	10.29	11.03	13.03	15.2	12.85	11.33	10.07	9.93	12.61	14.49	13.18	14.06	13.23	10.79	9.71	6.7	6
Expression	0.3441	0.4664	0.1378	4.2451	4.03	0.5532	1.5975	7.4943	4.2598	0.4478	0.2025	0.3335	1.3526	0.735	9.585	4.0721	38.6754	14.4779	0.5437	3.8195	0.5888	5.6403	0.3537	1.8801	0.662	0.98	0.2903	0.1628	2.0502	0.4149	0.7987	0.4799	0.1196	0.0266	0.1561	0.3684	0.9303	1.0251	0.1397	0.0435	0.1003	0.0573	0.1044	0.5897	1.1899	9.9183	16.8792

FIGURE 4